

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/538,767
Source: PCT
Date Processed by STIC: 06/21/2005

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 06/21/2005

PATENT APPLICATION: US/10/538,767

TIME: 13:49:24

Input Set : A:\SequenceListing.ST25.txt

Output Set: N:\CRF4\06172005\J538767.raw

```

4 <110> APPLICANT: Ottawa Health Research Institute
5     Megeney, Lynn
7 <120> TITLE OF INVENTION: MODULATION OF STEM CELL DIFFERENTIATION
8     BY MODULATION OF CASPASE-3 ACTIVITY
11 <130> FILE REFERENCE: 241-137PCT
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/538,767
C--> 14 <141> CURRENT FILING DATE: 2005-06-10
16 <150> PRIOR APPLICATION NUMBER: US 60/431,991
17 <151> PRIOR FILING DATE: 2002-12-10
19 <150> PRIOR APPLICATION NUMBER: US 60/431,990
20 <151> PRIOR FILING DATE: 2002-12-10
22 <160> NUMBER OF SEQ ID NOS: 10
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 835
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
W--> 32 <221> NAME/KEY:
33 <222> LOCATION:
34 <223> OTHER INFORMATION: human caspase-3 gene
36 <400> SEQUENCE: 1
37 aatggagaac actgaaaact cagtggattc aaaatccatt aaaaatttgg aaccaaagat 60
38 catacatgga agcgaatcaa tggactctgg aatatccctg gacaacagtt ataaaatgga 120
39 ttatcctgag atgggtttat gtataataat taataataag aattttcata aaagcactgg 180
40 aatgacatct cggctctggt cagatgtcga tgcagcaaac ctgagggaaa cattcagaaa 240
41 cttgaaatat gaagtcagga ataaaaatga tcttacacgt gaagaaattg tggaattgat 300
42 gcgtgatggt tctaaagaag atcacagcaa aaggagcagt tttgtttgtg tgcttctgag 360
43 ccatggtgaa gaaggaataa tttttggaac aaatggacct gttgacctga aaaaaataac 420
44 aaactttttc agaggggatc gttgtagaag tctaactgga aaacccaaac ttttcattat 480
45 tcaggcctgc cgtggtacag aactggactg tggcattgag acagacagtg gtgttgatga 540
46 tgacatggcg tgtcataaaa taccagtgga ggccgacttc ttgtatgcat actccacagc 600
47 acctggttat tattcttggc gaaattcaaa ggatggctcc tggttcatcc agtcgctttg 660
48 tgccatgctg aaacagtatg ccgacaagct tgaatttatg cacattctta cccgggttaa 720
49 ccgaaagggt gcaacagaat ttgagtcctt ttcctttgac gctacttttc atgcaaagaa 780
50 acagattcca tgtattgttt ccatgctcac aaaagaactc tattttttatc actaa      835
52 <210> SEQ ID NO: 2
53 <211> LENGTH: 277
54 <212> TYPE: PRT
55 <213> ORGANISM: Homo sapiens
57 <400> SEQUENCE: 2
58 Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu
59 1           5           10           15

```

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60 Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
61          20          25          30
62 Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
63          35          40          45
64 Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
65          50          55          60
66 Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
67 65          70          75          80
68 Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
69          85          90          95
70 Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
71          100          105          110
72 Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
73          115          120          125
74 Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
75          130          135          140
76 Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
77 145          150          155          160
78 Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
79          165          170          175
80 Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
81          180          185          190
82 Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
83          195          200          205
84 Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
85          210          215          220
86 Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
87 225          230          235          240
88 Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
89          245          250          255
90 His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
91          260          265          270
92 Leu Tyr Phe Tyr His
93          275

```

96 <210> SEQ ID NO: 3

97 <211> LENGTH: 1910

98 <212> TYPE: DNA

99 <213> ORGANISM: Homo sapiens

101 <220> FEATURE:

W--> 102 <221> NAME/KEY:

103 <222> LOCATION:

104 <223> OTHER INFORMATION: human MST1 gene

106 <400> SEQUENCE: 3

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107 ccggctgctg gcatcggcca tggagacggt acagctgagg aaccgcgcgc gccggcagct 60
108 gaaaaagtgt gatgaagata gtttaaccaa acaaccagaa gaagtatttg atgtcttaga 120
109 gaaacttgga gaagggctct atggcagcgt atacaaagct attcataaag agaccggcca 180
110 gattgttgct attaagcaag ttcctgtgga atcagacctc caggagataa tcaaagaaat 240
111 ctctataatg cagcaatgtg acagccctca tgtagtcaaa tattatggca gttattttaa 300
112 gaacacagac ttatggatcg ttatggagta ctgtggggct ggttctgtat ctgatatcat 360

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```

113 tcgattacga aataaaacgt taacagaaga tgaaatagct acaatattac aatcaactct 420
114 taagggactt gaataccttc attttatgag aaaaatacac cgagatatca aggcaggaaa 480
115 tattttgcta aatacagaag gacatgcaaa acttgtagat tttggggtag caggtcaact 540
116 tacagatacc atggccaagc ggaatacagt gataggaaca ccattttgga tggctccaga 600
117 agtgattcag gaaattggat acaactgtgt agcagacatc tgggccctgg gaataactgc 660
118 catagaaatg gctgaaggaa agcgccctta tgctgatatc catccaatga gggcaatctt 720
119 catgattcct acaaatectc ctcccacatt ccgaaaacca gagctatggc cagataactt 780
120 tacagatttt gtgaaacagt gtcttgtaaa gagccctgag cagagggcca cagccactca 840
121 gctcctgcag caccatttg tcaggagtgc caaaggagtg tcaatactgc gagacttaat 900
122 taatgaagcc atggatgtga aactgaaacg ccaggaatcc cagcagcggg aaatggacca 960
123 ggacgatgaa gaaaactcag aagaggatga aatggattct ggcacgatgg ttcgagcagt 1020
124 ggggtgatgag atgggactg tccgagtagc cagcaccatg actgatggag ccaatactat 1080
125 gattgagcac gatgacacgt tgccatcaca actgggcacc atggtgatca atgcagagga 1140
126 tgaggaagag gaaggaacta tgaaaagaag ggatgagacc atgcagcctg cgaaaccatc 1200
127 ctttcttgaa tattttgaac aaaaagaaaa ggaaaaccag atcaacagct ttggcaagag 1260
128 tgtacctggc cactgaaaa attcttcaga ttggaaaata ccacaggatg gagactacga 1320
129 gtttcttaag agttggacag tggaggacct tcagaagagg ctcttgccc tggaccccat 1380
130 gatggagcag gagattgaag agatccggca gaagtaccag tccaagcggc agcccatcct 1440
131 ggatgccata gaggctaaga agagacggca acaaaacttc tgagcaaggc caggctgtga 1500
132 gggcccccag tccaccagg ctttgggtga attctggatg gcttgctcat gttgttagc 1560
133 cagcaccttc tgctctgtcg tctctccaca gcacctttgt gaactcagga atgtgcgcca 1620
134 gtgggaaggg ctctcttgac agtcagcgtg ccactctgat gtgtgtatgt acattggtca 1680
135 ggtatattat ctcaaaggat ttatattggg cgacttttaa ctcagagttt taaacccag 1740
136 gaacagagac tcctagttag gtgatagctg ggaaagtttt acattgtctg ttttcttct 1800
137 cccaatagct ttcaattggt ctttctggaa gacttttaaa aaaatataaa tatgcatata 1860
138 tatatataaa ttataaatag attccccacg caggttggtg gcactctctgt 1910

```

140 <210> SEQ ID NO: 4

141 <211> LENGTH: 487

142 <212> TYPE: PRT

143 <213> ORGANISM: Homo sapiens

145 <400> SEQUENCE: 4

```

146 Met Glu Thr Val Gln Leu Arg Asn Pro Pro Arg Arg Gln Leu Lys Lys
147 1 5 10 15
148 Leu Asp Glu Asp Ser Leu Thr Lys Gln Pro Glu Glu Val Phe Asp Val
149 20 25 30
150 Leu Glu Lys Leu Gly Glu Gly Ser Tyr Gly Ser Val Tyr Lys Ala Ile
151 35 40 45
152 His Lys Glu Thr Gly Gln Ile Val Ala Ile Lys Gln Val Pro Val Glu
153 50 55 60
154 Ser Asp Leu Gln Glu Ile Ile Lys Glu Ile Ser Ile Met Gln Gln Cys
155 65 70 75 80
156 Asp Ser Pro His Val Val Lys Tyr Tyr Gly Ser Tyr Phe Lys Asn Thr
157 85 90 95
158 Asp Leu Trp Ile Val Met Glu Tyr Cys Gly Ala Gly Ser Val Ser Asp
159 100 105 110
160 Ile Ile Arg Leu Arg Asn Lys Thr Leu Thr Glu Asp Glu Ile Ala Thr
161 115 120 125
162 Ile Leu Gln Ser Thr Leu Lys Gly Leu Glu Tyr Leu His Phe Met Arg
163 130 135 140

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164 Lys Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Asn Thr Glu
165 145 150 155 160
166 Gly His Ala Lys Leu Ala Asp Phe Gly Val Ala Gly Gln Leu Thr Asp
167 165 170 175
168 Thr Met Ala Lys Arg Asn Thr Val Ile Gly Thr Pro Phe Trp Met Ala
169 180 185 190
170 Pro Glu Val Ile Gln Glu Ile Gly Tyr Asn Cys Val Ala Asp Ile Trp
171 195 200 205
172 Ser Leu Gly Ile Thr Ala Ile Glu Met Ala Glu Gly Lys Arg Pro Tyr
173 210 215 220
174 Ala Asp Ile His Pro Met Arg Ala Ile Phe Met Ile Pro Thr Asn Pro
175 225 230 235 240
176 Pro Pro Thr Phe Arg Lys Pro Glu Leu Trp Ser Asp Asn Phe Thr Asp
177 245 250 255
178 Phe Val Lys Gln Cys Leu Val Lys Ser Pro Glu Gln Arg Ala Thr Ala
179 260 265 270
180 Thr Gln Leu Leu Gln His Pro Phe Val Arg Ser Ala Lys Gly Val Ser
181 275 280 285
182 Ile Leu Arg Asp Leu Ile Asn Glu Ala Met Asp Val Lys Leu Lys Arg
183 290 295 300
184 Gln Glu Ser Gln Gln Arg Glu Met Asp Gln Asp Asp Glu Glu Asn Ser
185 305 310 315 320
186 Glu Glu Asp Glu Met Asp Ser Gly Thr Met Val Arg Ala Val Gly Asp
187 325 330 335
188 Glu Met Gly Thr Val Arg Val Ala Ser Thr Met Thr Asp Gly Ala Asn
189 340 345 350
190 Thr Met Ile Glu His Asp Asp Thr Leu Pro Ser Gln Leu Gly Thr Met
191 355 360 365
192 Val Ile Asn Ala Glu Asp Glu Glu Glu Glu Gly Thr Met Lys Arg Arg
193 370 375 380
194 Asp Glu Thr Met Gln Pro Ala Lys Pro Ser Phe Leu Glu Tyr Phe Glu
195 385 390 395 400
196 Gln Lys Glu Lys Glu Asn Gln Ile Asn Ser Phe Gly Lys Ser Val Pro
197 405 410 415
198 Gly Pro Leu Lys Asn Ser Ser Asp Trp Lys Ile Pro Gln Asp Gly Asp
199 420 425 430
200 Tyr Glu Phe Leu Lys Ser Trp Thr Val Glu Asp Leu Gln Lys Arg Leu
201 435 440 445
202 Leu Ala Leu Asp Pro Met Met Glu Gln Glu Ile Glu Glu Ile Arg Gln
203 450 455 460
204 Lys Tyr Gln Ser Lys Arg Gln Pro Ile Leu Asp Ala Ile Glu Ala Lys
205 465 470 475 480
206 Lys Arg Arg Gln Gln Asn Phe
207 485
210 <210> SEQ ID NO: 5
211 <211> LENGTH: 30
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:

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216 <223> OTHER INFORMATION: primer
218 <400> SEQUENCE: 5
219 atgaccatga ttacgaattc atggagacac 30
221 <210> SEQ ID NO: 6
222 <211> LENGTH: 30
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: primer
229 <400> SEQUENCE: 6
230 cactctagat taattaaaaa aatagagttc 30
232 <210> SEQ ID NO: 7
233 <211> LENGTH: 268
234 <212> TYPE: PRT
235 <213> ORGANISM: Homo sapiens
237 <400> SEQUENCE: 7
238 Ser Lys Ser Ile Lys Asn Leu Glu Pro Lys Ile Ile His Gly Ser Glu
239 1 5 10 15
240 Ser Met Asp Ser Gly Ile Ser Leu Asp Asn Ser Tyr Lys Met Asp Tyr
241 20 25 30
242 Pro Glu Met Gly Leu Cys Ile Ile Ile Asn Asn Lys Asn Phe His Lys
243 35 40 45
244 Ser Thr Gly Met Thr Ser Arg Ser Gly Thr Asp Val Asp Ala Ala Asn
245 50 55 60
246 Leu Arg Glu Thr Phe Arg Asn Leu Lys Tyr Glu Val Arg Asn Lys Asn
247 65 70 75 80
248 Asp Leu Thr Arg Glu Glu Ile Val Glu Leu Met Arg Asp Val Ser Lys
249 85 90 95
250 Glu Asp His Ser Lys Arg Ser Ser Phe Val Cys Val Leu Leu Ser His
251 100 105 110
252 Gly Glu Glu Gly Ile Ile Phe Gly Thr Asn Gly Pro Val Asp Leu Lys
253 115 120 125
254 Lys Ile Thr Asn Phe Phe Arg Gly Asp Arg Cys Arg Ser Leu Thr Gly
255 130 135 140
256 Lys Pro Lys Leu Phe Ile Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp
257 145 150 155 160
258 Cys Gly Ile Glu Thr Asp Ser Gly Val Asp Asp Asp Met Ala Cys His
259 165 170 175
260 Lys Ile Pro Val Glu Ala Asp Phe Leu Tyr Ala Tyr Ser Thr Ala Pro
261 180 185 190
262 Gly Tyr Tyr Ser Trp Arg Asn Ser Lys Asp Gly Ser Trp Phe Ile Gln
263 195 200 205
264 Ser Leu Cys Ala Met Leu Lys Gln Tyr Ala Asp Lys Leu Glu Phe Met
265 210 215 220
266 His Ile Leu Thr Arg Val Asn Arg Lys Val Ala Thr Glu Phe Glu Ser
267 225 230 235 240
268 Phe Ser Phe Asp Ala Thr Phe His Ala Lys Lys Gln Ile Pro Cys Ile
269 245 250 255
270 Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Tyr His

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VERIFICATION SUMMARY

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TIME: 13:49:25

Input Set : A:\SequenceListing.ST25.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:32 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1

L:102 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3